



SEQUENCE LISTING

<110> Dale Umetsu
Rosemarie DeKruyff
Jennifer McIntire
Gordon Freeman

<120> T CELL REGULATORY GENES ASSOCIATED WITH
IMMUNE DISEASE

<130> STAN-235CIP

<150> 60/302,344

<151> 2001-06-29

<150> 10/188,012

<151> 2002-07-01

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 305

<212> PRT

<213> M. musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-1 BALB/c allele

<400> 1

Met	Asn	Gln	Ile	Gln	Val	Phe	Ile	Ser	Gly	Leu	Ile	Leu	Leu	Leu	Pro
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			20					25					30		
Val	Thr	Leu	Pro	Cys	Thr	Tyr	Ser	Thr	Tyr	Arg	Gly	Ile	Thr	Thr	Thr
		35					40					45			
Cys	Trp	Gly	Arg	Gly	Gln	Cys	Pro	Ser	Ser	Ala	Cys	Gln	Asn	Thr	Leu
	50					55					60				
Ile	Trp	Thr	Asn	Gly	His	Arg	Val	Thr	Tyr	Gln	Lys	Ser	Ser	Arg	Tyr
65					70					75				80	
Asn	Leu	Lys	Gly	His	Ile	Ser	Glu	Gly	Asp	Val	Ser	Leu	Thr	Ile	Glu
				85					90					95	
Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile
			100					105					110		
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys
	115						120					125			
Pro	Glu	Ile	Pro	Thr	Arg	Pro	Pro	Thr	Arg	Pro	Thr	Thr	Thr	Arg	Pro
	130					135					140				
Thr	Ala	Thr	Gly	Arg	Pro	Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val
145					150					155				160	
Pro	Thr	Ser	Ile	Arg	Val	Ser	Thr	Ser	Thr	Pro	Pro	Thr	Ser	Thr	His
				165					170					175	
Thr	Trp	Thr	His	Lys	Pro	Glu	Pro	Thr	Thr	Phe	Cys	Pro	His	Glu	Thr
			180					185					190		
Thr	Ala	Glu	Val	Thr	Gly	Ile	Pro	Ser	His	Thr	Pro	Thr	Asp	Trp	Asn
	195						200					205			
Gly	Thr	Val	Thr	Ser	Ser	Gly	Asp	Thr	Trp	Ser	Asn	His	Thr	Glu	Ala

210		215		220
Ile Pro Pro Gly Lys	Pro Gln Lys Asn Pro Thr	Lys Gly Phe Tyr Val		
225	230	235	240	
Gly Ile Cys Ile Ala	Ala Leu Leu Leu Leu Leu	Val Ser Thr Val		
	245	250	255	
Ala Ile Thr Arg Tyr	Ile Leu Met Lys Arg Lys	Ser Ala Ser Leu Ser		
	260	265	270	
Val Val Ala Phe Arg	Val Ser Lys Ile Glu Ala	Leu Gln Asn Ala Ala		
	275	280	285	
Val Val His Ser Arg	Ala Glu Asp Asn Ile Tyr	Ile Val Glu Asp Arg		
	290	295	300	
Pro				
305				

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 <211> 918
 <212> DNA
 <213> Mus musculus

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 tcttatgtgg aagtaaaggg ggtagtgggt caccctgtca cacttccatg tacttactca 120
 acatatcgtg gaatcacaaac gacatgttgg ggccgagggc aatgcccata ttctgcttgt 180
 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtccgtac 240
 aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300
 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360
 gtgacctttt cattgcaagt taaaccagag attcccacac gtccctccaa aagaccaca 420
 actacaaggc ccacagctac aggaagaccc acgactatct caacaagatc cacacatgta 480
 ccaacatcaa tcagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
 aaaccagaac ccactacatt ttgtcccat gagacaacag ctgaggtgac aggaatccca 600
 tcccatactc ctacagactg gaatggcact gtgacatcct caggagatac ctggagtaat 660
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 ggcactctgca tcgcagccct gctgctactg ctccttgtga gcaccgtggc tatcaccagg 780
 tacatactta tgaaggaa gtcagcatct ctaagcgtgg ttgccttccg tgtctctaag 840
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<210> 3
 <211> 282
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(282)
 <223> TIM-1, C.D2 ES-HBA and DBA/2J allele

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 20 25 30
 Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr
 35 40 45
 Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
 50 55 60
 Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
 65 70 75 80
 Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
 85 90 95

Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile
		100						105					110		
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys
		115					120					125			
Pro	Glu	Ile	Pro	Thr	Arg	Pro	Pro	Arg	Arg	Pro	Thr	Thr	Thr	Arg	Pro
		130				135					140				
Thr	Ala	Thr	Gly	Arg	Pro	Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val
145					150					155				160	
Pro	Thr	Ser	Thr	Arg	Val	Ser	Thr	Ser	Thr	Pro	Pro	Thr	Ser	Thr	His
				165				170					175		
Thr	Trp	Thr	His	Lys	Pro	Asp	Trp	Asn	Gly	Thr	Val	Thr	Ser	Ser	Gly
			180					185				190			
Asp	Thr	Trp	Ser	Asn	His	Thr	Glu	Ala	Ile	Pro	Pro	Gly	Lys	Pro	Gln
		195					200					205			
Lys	Asn	Pro	Thr	Lys	Gly	Phe	Tyr	Val	Gly	Ile	Cys	Ile	Ala	Ala	Leu
	210					215					220				
Leu	Leu	Leu	Leu	Leu	Val	Ser	Thr	Val	Ala	Ile	Thr	Arg	Tyr	Ile	Leu
225					230					235				240	
Met	Lys	Arg	Lys	Ser	Ala	Ser	Leu	Ser	Val	Val	Ala	Phe	Arg	Val	Ser
				245				250					255		
Lys	Ile	Glu	Ala	Leu	Gln	Asn	Ala	Ala	Val	Val	His	Ser	Arg	Ala	Glu
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Asp	Asn	Ile	Tyr	Ile	Val	Glu	Asp	Arg	Pro						
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<210> 4
 <211> 849
 <212> DNA
 <213> Mus musculus

<400> 4
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 acatatcgtg gaatcacaac gacatgttgg ggccgagggc aatgcccatc ttctgcttgt 180
 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtac 240
 aacttaaagg ggcataattc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300
 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360
 gtgacctttt cattgcaagt taaaccagag attcccacac gtctccaag aagaccaca 420
 actacaaggc ccacagctac aggaagacc acgactattt caacaagatc cacacatgta 480
 ccaacatcaa ccagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
 aaaccagact ggaatggcac tgtgacatcc tcaggagata cctggagtaa tcacactgaa 600
 gcaatccctc caggaagcc gcagaaaaac cctactaagg gcttctatgt tggcatctgc 660
 atcgcagccc tgctgtact gctccttgtg agcaccgtgg ctatcaccag gtacatactt 720
 atgaaaagga agtcagcatc tctaagcgtg gttgccttcc gtgtctctaa gattgaagct 780
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 agaccttga 849

<210> 5
 <211> 305
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(305)
 <223> TIM-2 BALB/c allele

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Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
 20 25 30
 Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
 35 40 45
 Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
 50 55 60
 Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
 65 70 75 80
 Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
 85 90 95
 Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
 100 105 110
 Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
 115 120 125
 Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
 130 135 140
 Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
 145 150 155 160
 Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
 165 170 175
 Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
 180 185 190
 Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
 195 200 205
 Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
 210 215 220
 Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
 225 230 235 240
 Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
 245 250 255
 Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
 260 265 270
 Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
 275 280 285
 Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
 290 295 300
 Ser
 305

<210> 6
 <211> 958
 <212> DNA
 <213> Mus musculus

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 tcaccctgtc acacttccat gtattttattc gacacacctt ggtggaatcg ttcctatgtg 180
 ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240
 atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300
 aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtgggtccct attgctgtgt 360
 agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
 ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
 atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540
 cacagagacc tacaacaccag aggccactac attttatcca gatcagacta cagctgaggt 600
 gacagaaacc ttaccctcta ctctgcaga ctggcataac actgtgacat cctcagatga 660
 cccttgggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720
 gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780
 ggttatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct ttgttgctt 840
 ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900

ccaggtctac attattgaag acactcctta ccctgaagaa gaggcttagt gcctctac 958

<210> 7

<211> 305

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-2, C.D2 ES-HBA and DBA/2J allele

<400> 7

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Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro
 1          5          10          15
Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
 20          25          30
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
 35          40          45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
 50          55          60
Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
 65          70          75          80
Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
 85          90          95
Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
100          105          110
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
115          120          125
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
130          135          140
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
145          150          155          160
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
165          170          175
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
180          185          190
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
195          200          205
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
210          215          220
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
225          230          235          240
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
245          250          255
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
260          265          270
Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
275          280          285
Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
290          295          300
Ser
305

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<210> 8

<211> 958

<212> DNA

<213> Mus musculus

<400> 8

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tcaccctgtc acacttccat gtattttattc gacacacctt ggtggaatcg ttcctatgtg 180
ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240
atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300
aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtcctt attgctgtgt 360
agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540
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ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900
ccaggtctac attattgaag acactcctta ccccgaaaga gattcctagt gcctctac 958

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<210> 9

<211> 281

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(281)

<223> TIM-3 BALB/c allele

<400> 9

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Leu Leu Ala Arg Ser Leu Glu Asp Gly Tyr Lys Val Glu Val Gly Lys
          20           25           30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu
          35           40           45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
          50           55           60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65           70           75           80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
          85           90           95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
          100          105          110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
          115          120          125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
          130          135          140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145          150          155          160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
          165          170          175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
          180          185          190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
          195          200          205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
210          215          220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
225          230          235          240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
          245          250          255
Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr

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260
Cys Tyr Val Asn Ser Gln Gln Pro Ser
275

265
Pro Ser
280

270

<210> 10
<211> 2725
<212> DNA
<213> Mus musculus

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agttacactc tacctacatc tgggacactt gtgcctatgt gctggggcaa gggattctgt 240
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tcagaaggct ggagcagaag cgtggagagt tcaggagcac tgtgcccac actgccagac 2040
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<210> 11
<211> 281
<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(281)

<223> TIM-3, C.D2 ES-HBA and DBA/2J allele

<400> 11

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Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
 20           25           30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
 35           40           45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
 50           55           60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
 65           70           75           80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
 85           90           95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
 100          105          110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
 115          120          125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
 130          135          140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
 145          150          155          160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
 165          170          175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
 180          185          190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
 195          200          205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
 210          215          220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
 225          230          235          240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
 245          250          255
Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr
 260          265          270
Cys Tyr Val Asn Ser Gln Gln Pro Ser
 275          280
```

<210> 12

<211> 862

<212> DNA

<213> Mus musculus

<400> 12

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ccctcccaa gtactcatgt ttccaggtct taccctcaac tgtgtcctgc tgctgctgca 60
actactactt gcaaggtcat tggaaaatgc ttatgtgttt gaggttggtg agaatgccta 120
tctgccctgc agttacactc tatctacacc tggggcactt gtgcctatgt gctggggcaa 180
gggattctgt ccttggtcac agtgtaccaa cgagttgctc agaactgatg aaagaaatgt 240
gacatatcag aaatccagca gataccagct aaagggcgat ctcaacaaag gagacgtgtc 300
tctgatcata aagaatgtga ctctggatga ccatgggacc tactgctgca ggatacagtt 360
ccctggtctt atgaatgata aaaaattaga actgaaatta gacatcaaag cagccaaggt 420
cactccagct cagactgcc atggggactc tactacagct tctccaagaa ccctaaccac 480
ggagagaaat gggttcagaga cacagacact ggtgaccctc cataataaca atggaacaaa 540
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```

aatttcacaca tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgctatcca 600
cattggagtg ggagtcctctg ctgggttgac cctggcactt atcattgggtg tcttaatcct 660
taaattggtat tctgtgaaga aaaagaagtt atcgagtttg agccttatta cactggccaa 720
cttgccctcca ggagggttg gaaatgcagg agcagtcagg attcgctctg aggaaaatat 780
ctacaccatc gaggagaacg tatatgaagt ggagaattca aatgagtact actgctacgt 840
caacagccag cagccatcct ga 862

```

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<210> 13
<211> 345
<212> PRT
<213> Mus musculus

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<220>
<221> VARIANT
<222> (1)...(345)
<223> TIM-4, BALB/c allele

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```

<400> 13
Met Ser Lys Gly Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
1          5          10          15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20          25          30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35          40          45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50          55          60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65          70          75          80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85          90          95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100          105          110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115          120          125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
130          135          140
Thr Thr Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
145          150          155          160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
165          170          175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180          185          190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195          200          205
Ser Ala Ile Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210          215          220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225          230          235          240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245          250          255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260          265          270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
275          280          285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290          295          300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305          310          315          320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325          330          335
Asp Asp Glu Asp Gly Ile Phe Thr Leu

```

<210> 14
 <211> 1032
 <212> DNA
 <213> Mus musculus

<400> 14
 atgtccaagg ggcttctcct cctctggctg gtgacggagc tctgggtggct ttatctgaca 60
 ccagctgcct cagaggatac aataataggg tttttggggc agccgggtgac tttgccttgt 120
 cattacctct cgtgggtccca gagccgcaac agtatgtgct ggggcaaagg ttcatgtccc 180
 aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
 tcaacaaaat atacactttt ggggaagggtc cagtttggtg aagtgtcctt gaccatctca 300
 aacaccaatc gaggtgacag tgggggtgtac tgctgccgta tagagggtgcc tggctgggttc 360
 aatgatgtca agaagaatgt gcgcttgagg ctgaggagag ccacaacaac caaaaaacca 420
 acaacaacca cccggccaac caccacccct tatgtaacca ccaccacccc agagctgctt 480
 ccaacaacag tcatgaccac atctgttctt ccaaccacca caccacccca gacactagcc 540
 accactgcct tcagtacagc agtgaccacg tgcccctcaa caacacctgg ctcttcttca 600
 caagaaacca caaaaggggtc cgccatcact acagaatcag aaactctgcc tgcattccaat 660
 cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gcccacaggc 720
 tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
 acaagtgagt ctttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
 ttgatcattg cctgctgtgt gggatttgtg ctaatggtgt tattgtttct ggcgtttctc 900
 cttcgaggga aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
 gaagatagt acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
 ttcactctct ga 1032

<210> 15
 <211> 345
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(345)
 <223> C.D2 ES-HBA and DBA/2J allele

<400> 15
 Met Ser Lys Gly Leu Leu Leu Trp Leu Val Met Glu Leu Trp Trp
 1 5 10 15
 Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
 20 25 30
 Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
 35 40 45
 Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
 50 55 60
 Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
 65 70 75 80
 Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
 85 90 95
 Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
 100 105 110
 Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
 115 120 125
 Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
 130 135 140
 Thr Thr Arg Pro Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
 145 150 155 160
 Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
 165 170 175

Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
 180 185 190
 Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
 195 200 205
 Ser Ala Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
 210 215 220
 Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
 225 230 235 240
 Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
 245 250 255
 Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
 260 265 270
 Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
 275 280 285
 Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
 290 295 300
 Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
 305 310 315 320
 Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
 325 330 335
 Asp Asp Glu Asp Gly Ile Phe Thr Leu
 340 345

<210> 16
 <211> 1032
 <212> DNA
 <213> Mus musculus

<400> 16
 atgtccaagg ggcttctcct cctctggctg gtgatggagc tctgggtggct ttatctgaca 60
 ccagctgcct cagaggatac aataataggg tttttggggc agccggtgac tttgccttgt 120
 cattacctct cgtgggtccca gagccgcaac agtatgtgct ggggcaaagg ttcatgtccc 180
 aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
 tcaacaaaat atacactttt ggggaaggte cagtttgggtg aagtgtcctt gaccatctca 300
 aacaccaatc gaggtgacag tggggtgtac tgctgccgta tagagggtgcc tggctggttc 360
 aatgatgtca agaagaatgt gcgcttggag ctgaggagag ccacaacaac caaaaaacca 420
 acaacaacca cccggccaac caccaccctt tatgtaacca ccaccacccc agagctgctt 480
 ccaacaacag tcatgaccac atctgttctt ccaaccacca caccaccca gacactagcc 540
 accactgcct tcagtacagc agtgaccacg tgcccctcaa caacacctgg ctcttctca 600
 caagaaacca caaaagggc cgccttcact acagaatcag aaactctgcc tgcattcaat 660
 cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gccacaggc 720
 tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
 acaagtgagt ctttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
 ttgatcattg cctgctgtgt gggatttgtg ctaatgggtg tattgtttct ggcgtttctc 900
 cttcgaggga aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
 gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
 ttcactctct ga 1032

<210> 17
 <211> 359
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(360)
 <223> TIM-1 allele 1

<400> 17
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp

1				5				10					15				
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Glu	Ala	Gly	Pro	Ser	Val			
			20					25				30					
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn		
		35					40					45					
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr		
	50					55					60						
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu		
65					70					75					80		
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala		
				85					90					95			
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp		
			100					105					110				
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys		
	115						120					125					
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val		
	130					135					140						
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr	Thr		
145					150						155				160		
Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr		
				165					170					175			
Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro	Thr	Thr	Thr	Ser	Ile	Pro		
			180					185					190				
Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Thr	Val	Ser	Thr	Phe	Val	Pro		
	195						200					205					
Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	Val	Ala	Thr	Ser	Pro		
	210					215					220						
Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr	Thr	Leu	Gln	Gly	Ala		
225					230					235				240			
Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr	Ser	Tyr	Thr	Thr	Asp		
				245					250					255			
Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly	Leu	Trp	Asn	Asn	Asn		
		260						265					270				
Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu	Thr	Ala	Asn	Thr	Thr		
	275						280					285					
Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val	Leu	Val	Leu	Leu	Ala		
	290					295					300						
Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe	Phe	Lys	Lys	Glu	Val		
305					310					315				320			
Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln	Ile	Lys	Ala	Leu	Gln		
				325					330					335			
Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp	Asn	Ile	Tyr	Ile	Glu		
			340					345					350				
Asn	Ser	Leu	Tyr	Ala	Thr	Asp											
		355															

<210> 18
 <211> 1080
 <212> DNA
 <213> H. sapiens

<400> 18
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60
 tctgtaaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgccac ctacagtggg 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtcgtacagt 300
 ggcgatatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcacaggta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480

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gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540
acgacaacga gcgtttccaaac gacaacgagc attccaacaa caacaagtgt tccagtgaaca 600
acaacggtct ctacctttgt tcttccaatg cctttgcccc ggacagaacca tgaaccagta 660
gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
ataaggagag aaccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900
gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960
caacaactaa gtgttttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

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<210> 19
<211> 359
<212> PRT
<213> H. sapiens

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<220>
<221> VARIANT
<222> (1)...(359)
<223> TIM-1, allele 2

```

```

<400> 19
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1          5          10          15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
          20          25          30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
          35          40          45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
          50          55          60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
          65          70          75          80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
          85          90          95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
          100          105          110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
          115          120          125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
          130          135          140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr
          145          150          155          160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr
          165          170          175
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
          180          185          190
Thr Thr Thr Ser Val Pro Val Thr Thr Ala Val Ser Thr Phe Val Pro
          195          200          205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
          210          215          220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
          225          230          235          240
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
          245          250          255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
          260          265          270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
          275          280          285
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala
          290          295          300

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Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val
 305 310 315 320
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln
 325 330 335
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu
 340 345 350
 Asn Ser Leu Tyr Ala Thr Asp
 355

<210> 20
 <211> 1080
 <212> DNA
 <213> H. sapiens

<400> 20
 atgcacccctc aagtgggtcat cttaagccctc atccctacatc tggcagattc tgtagctggt 60
 tctgttaaagg ttgggtggaga ggcagggtcca tctgtcacac taccctgccca ctacagtggg 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatat ttgtgccctg tgagcacogt ggggtggttca atgacatgaa aatcacgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactggt ccaacgacaa cgactgttcc aacgacaact 480
 gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540
 acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgcga 600
 acagcgggtc ctacctttgt tctccaatg cctttgccca ggcagaacca tgaaccagta 660
 gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
 ataaggagag aaccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
 gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
 agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900
 gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggagggt 960
 caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
 aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

<210> 21
 <211> 365
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(365)
 <223> TIM-1, allele 3

<400> 21
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110

Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
	115						120					125			
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
	130					135						140			
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Met	Thr	Thr
	145				150					155					160
Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr
			165						170					175	
Thr	Thr	Val	Pro	Thr	Thr	Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro
			180					185					190		
Thr	Thr	Thr	Ser	Ile	Pro	Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ala
			195				200					205			
Val	Ser	Thr	Phe	Val	Pro	Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu
	210					215					220				
Pro	Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro
	225				230					235					240
Thr	Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu
			245						250					255	
Tyr	Ser	Tyr	Thr	Thr	Asp	Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp
		260					265						270		
Gly	Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu
	275					280						285			
Leu	Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser
	290					295					300				
Val	Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr
	305				310					315					320
Phe	Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu
			325					330						335	
Gln	Ile	Lys	Ala	Leu	Gln	Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu
		340						345					350		
Asp	Asn	Ile	Tyr	Ile	Glu	Asn	Ser	Leu	Tyr	Ala	Thr	Asp			
	355						360					365			

<210> 22
 <211> 1098
 <212> DNA
 <213> H. sapiens

<400> 22
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60
 tctgtaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgccca ctacagtggga 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480
 actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
 acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
 acaagtgttc cagtgcacaac arcggtctct acctttgttc ctccaatgcc tttgccagg 660
 cagaacctatg aaccagtagc cacttcacca tcttcacctc agccagcaga aaccaccct 720
 acgacactgc agggagcaat aaggagagaa cccaccagct caccattgta ctcttacaca 780
 acagatggga atgacaccgt gacagagtct tcagatggcc tttggaataa caatcaaact 840
 caactgttcc tagaacatag tctactgacg gccaatacca cttaaaggaa ctatgctgga 900
 gtctgtattt ctgtcttggt gcttcttgct cttttgggtg tcatcattgc caaaaagtat 960
 ttcttcaaaa aggaggttca acaactaagt gtttcattta gcagccttca aattaaagct 1020
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 ctttatgccca cggactaa 1098

<210> 23

<210>	24
<211>	1079
<212>	DNA

<213> H. sapiens

<400> 24

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gctgtcacat caatgtgctg gaatagagggc tcatgtttctc tattcacatg ccaaaatggc 180
attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
gtcacgactg ttcgaacgag caccactggt ccaacgacaa cgactgttcc aacgacaact 480
gttccaacaa caatgagcat tccaacgaca acggactggt ccgacgacaa tgactgtttc 540
aacgacaacg agcgtttccaa cgacaacgag cattccaaca acaacaagtg ttccagtgaac 600
aacatgtctc tacctttgtt cctccaatgc ctttgcccag gcagaacat gaaccagtag 660
ccacttcacc atcttcacct cagccagcag aaaccacccc tacgacactg caggagacaa 720
taaggagaga acccaccagc tcaccattgt actcttacac aacagatggg aatgacaccg 780
tgacagagtc ttcagatggc ctttgarta acaatcaaac tcaactgttc ctagaacata 840
gtctactgac ggccaatacc actaaaggaa tctatgctgg agtctgtatt tctgtcttgg 900
tgcttcttgc tcttttgggt gtcattcattg ccaaaaagta tttcttcaaa aaggagggtc 960
aacaactaag tgtttcattt agcagccttc aaattaaagc tttgcaaaat gcagttgaaa 1020
aggaagtcca agcagaagac aatatctaca ttgagaatag tctttatgcc acggactaa 1079
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<210> 25

<211> 364

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(364)

<223> TIM-1 allele 5

<400> 25

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Met His Pro Gln Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
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Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20          25          30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35          40          45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50          55          60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65          70          75          80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85          90          95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100          105          110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115          120          125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130          135          140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Met Thr Thr
145          150          155          160
Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165          170          175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro
180          185          190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Val
195          200          205
Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
210          215          220
```

Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr
225					230					235					240
Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr
				245					250						255
Ser	Tyr	Thr	Thr	Asp	Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly
			260					265						270	
Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu
		275					280					285			
Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val
	290					295					300				
Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe
305					310					315					320
Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln
				325					330						335
Ile	Lys	Ala	Leu	Gln	Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp
			340					345					350		
Asn	Ile	Tyr	Ile	Glu	Asn	Ser	Leu	Tyr	Ala	Thr	Asp				
		355					360								

<210> 26
 <211> 1095
 <212> DNA
 <213> H. sapiens

<400> 26
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 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcacctga 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactggt ccaacgacaa cgactgttcc aatgacaacg 480
 actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
 acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
 agtgttccag tgacaacaac ggtctctacc tttgttctc caatgccttt gccacggcag 660
 aaccatgaac cagtagccac ttcaccatct tcacctcagc cagcagaaac ccaccctacg 720
 acactgcagg gagcaataag gagagaaccc accagctcac cattgtactc ttacacaaca 780
 gatgggaatg acaccgtgac agagtcttca gatggccttt ggaataacaa tcaaaactcaa 840
 ctgttcttag aacatagtct actgacggcc aataccacta aaggaatcta tgctggagtc 900
 tgtatttctg tcttgggtgct tcttgtctct ttgggtgtca tcattgccaa aaagtatttc 960
 ttcaaaaagg aggttcaaca actaagtgtt tcatttagca gccttcaaat taaagctttg 1020
 caaaatgcag ttgaaaagga agtccaagca gaagacaata tctacattga gaatagtctt 1080
 tatgccacgg actaa 1095

<210> 27
 <211> 364
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(364)
 <223> TIM-1, allele 6

<400> 27
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30

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<210> 28
<211> 1099
<212> DNA
<213> H. sapiens
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gctgtcacat	caatgtgctg	gaatagaggc	tcatgttctc	tattcacatg	ccaaaatggc	180
attgtctgga	ccaatggaac	ccacgtcacc	tatcggaagg	acacacgcta	taagctattg	240
ggggaccttt	caagaaggga	tgtctctttg	accatagaaa	atacagctgt	gtctgacagt	300
ggcgatatatt	gttgccgtgt	tgagcaccgt	gggtggttca	atgacatgaa	aatcaccgta	360
tcattggaga	ttgtgccacc	caaggtcacg	actactccaa	ttgtcacaa	tgttccaacc	420
gtcacgactg	ttcgaacag	caccactgtt	ccaacgacaa	cgactgttcc	aatgacaacc	480
gactgttcca	acgacaactg	ttccaacaac	aatgagcatt	ccaacgacaa	cgactgttcc	540
gacgacaatg	actgtttcaa	cgacaacgag	cgttccaacg	acaacgagca	ttccaacaac	600
aacaagtgtt	ccagtgcaca	caacgggtctc	tacctttgtt	cctccaatgc	ctttgccag	660

gcagaacccat gaaccagtag ccacttcacc atcttcacct cagccagcag aaacccaccc 720
 tacgacactg cagggagcaa taaggagaga acccaccagc tcaccattgt actcttacac 780
 aacagatggg gatgacaccg tgacagagtc ttcagatggc ctttggaata acaatcaaac 840
 tcaactgttc ctagaacata gtctactgac ggccaatacc actaaaggaa tctatgctgg 900
 agtctgtatt tctgtcttgg tgcttcttgc tcttttgggt gtcattcattg ccaaaaagta 960
 tttcttcaaaa aaggagggttc aacaactaag tgtttcattt agcagccttc aaattaaagc 1020
 tttgcaaaat gcagttgaaa aggaagtcca agcagaagac aatatctaca ttgagaatag 1080
 tctttatgcc acggactaa 1099

<210> 29
 <211> 301
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(301)
 <223> TIM-3, allele 1

<400> 29
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
 20 25 30
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
 35 40 45
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
 50 55 60
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
 65 70 75 80
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
 85 90 95
 Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
 100 105 110
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
 115 120 125
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
 130 135 140
 Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160
 Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175
 Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190
 Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
 195 200 205
 Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
 210 215 220
 Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
 225 230 235 240
 Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
 245 250 255
 Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
 260 265 270
 Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
 275 280 285
 Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
 290 295 300

<210> 30

<211> 1116
 <212> DNA
 <213> H. sapiens

<400> 30
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 ttttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120
 tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
 ccagccgccc cagggaaacct cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
 gaatgtggca acgtgggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300
 tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360
 ctagcagaca gtgggatcta ctgctgccgg atccaaatcc caggcataat gaatgatgaa 420
 aaattttaacc tgaagttggg catcaaacca gccaaaggtca cccctgcacc gactctgcag 480
 agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540
 acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600
 gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660
 ggcactctaca tcggagcagg gatctgtgct gggctggctc tggtctctat cttcggcgct 720
 ttaattttca aatggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780
 ttggccaacc tccctccctc aggattggca aatgcagtag cagaggggaat tcgctcagaa 840
 gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900
 tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcca 960
 tagatccaac caccttattt ttgagcttgg tgttttgcct ttttcagaaa ctatgagctg 1020
 tgtcacctga ctggttttgg aggttctgtc cactgctatg gagcagagtt ttcccatttt 1080
 cagaagataa tgactcacat gggaattgaa ctggga 1116

<210> 31
 <211> 301
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(301)
 <223> TIM-3, allele 2

<400> 31
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
 20 25 30
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
 35 40 45
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
 50 55 60
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
 65 70 75 80
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
 85 90 95
 Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
 100 105 110
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
 115 120 125
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
 130 135 140
 Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160
 Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175
 Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190
 Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly

195					200					205						
Ile	Cys	Ala	Gly	Leu	Ala	Leu	Ala	Leu	Ile	Phe	Gly	Ala	Leu	Ile	Phe	
210					215					220						
Lys	Trp	Tyr	Ser	His	Ser	Lys	Glu	Lys	Ile	Gln	Asn	Leu	Ser	Leu	Ile	
225					230					235					240	
Ser	Leu	Ala	Asn	Leu	Pro	Pro	Ser	Gly	Leu	Ala	Asn	Ala	Val	Ala	Glu	
245					250					255						
Gly	Ile	Arg	Ser	Glu	Glu	Asn	Ile	Tyr	Thr	Ile	Glu	Glu	Asn	Val	Tyr	
260					265					270						
Glu	Val	Glu	Glu	Pro	Asn	Glu	Tyr	Tyr	Cys	Tyr	Val	Ser	Ser	Arg	Gln	
275					280					285						
Gln	Pro	Ser	Gln	Pro	Leu	Gly	Cys	Arg	Phe	Ala	Met	Pro				
290					295					300						

<210> 32
 <211> 1116
 <212> DNA
 <213> H. sapiens

<400> 32
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 tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
 ccagccgccc cagggaaacct cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
 gaatgtggca acgtggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300
 tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360
 ctagcagaca gtgggatcta ctgctgccgg atccaaatcc caggcataat gaatgatgaa 420
 aaattttaacc tgaagtttgt catcaaacca gccaaaggtca cccctgcacc gactcggcag 480
 agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg ccagcagag 540
 acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600
 gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660
 ggcattctaca tcggagcagg gatctgtgct gggctggctc tggctcttat cttcggcgct 720
 ttaattttca aatggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780
 ttggccaacc tccctccctc aggattggca aatgcagtag cagagggaat tcgctcagaa 840
 gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900
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 tagatccaac caccttattt ttgagcttgg tgttttgtct ttttcagaaa ctatgagctg 1020
 tgtcacctga ctgggttttg aggttctgtc cactgctatg gagcagagtt ttcccatttt 1080
 cagaagataa tgactcacat gggaattgaa ctggga 1116

<210> 33
 <211> 378
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(378)
 <223> TIM-4, allele 1

<400> 33
 Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
 1 5 10 15
 Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
 20 25 30
 Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
 35 40 45
 Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
 50 55 60
 Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys

65					70					75				80	
Ser	Ala	Lys	Tyr	Arg	Leu	Gln	Gly	Thr	Ile	Pro	Arg	Gly	Asp	Val	Ser
				85					90					95	
Leu	Thr	Ile	Leu	Asn	Pro	Ser	Glu	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys
			100					105					110		
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Ile	Asn	Val	Arg
		115					120					125			
Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr	Thr	Thr	His	Arg	Thr	Ala	Thr	Thr
	130					135					140				
Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr	Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met
145						150				155					160
Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro	Thr	Thr	Val	Val	Thr	Thr	Pro	Asp
			165					170						175	
Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln	Met	Thr	Thr	Ile	Ala	Val	Phe	Thr
			180					185					190		
Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu	Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu
	195						200					205			
Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu	Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu
	210					215					220				
Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu	Pro	Ser	Asp	Ser	Trp	Ser	Ser	Ala
225						230				235					240
Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val	Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys
			245					250						255	
Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	His	Val	Ser	Met	Trp	Lys	Thr	Ser
			260					265					270		
Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro
		275					280					285			
Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	Gly	Gln	Met	Asp	Gly	Ile	Pro	Met
	290					295				300					
Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala
305					310					315					320
Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	Ala	Leu	Phe	Val	Ala	Phe	Leu	Leu
			325					330						335	
Arg	Gly	Lys	Leu	Met	Glu	Thr	Tyr	Cys	Ser	Gln	Lys	His	Thr	Arg	Leu
			340					345					350		
Asp	Tyr	Ile	Gly	Asp	Ser	Lys	Asn	Val	Leu	Asn	Asp	Val	Gln	His	Gly
	355						360					365			
Arg	Glu	Asp	Glu	Asp	Gly	Leu	Phe	Thr	Leu						
	370					375									

<210> 34
 <211> 1156
 <212> DNA
 <213> H. sapiens

<400> 34
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 ctgtactcat cctggtctca caacagcaac agcatgtgct gggggaaaga ccagtgcccc 180
 tactccggtt gcaaggaggc gtcacccgc actgatggaa tgagggtgac ctcaagaaag 240
 tcagcaaaat atagacttca ggggactatc ccgagagggtg atgtctcctt gaccatctta 300
 aaccccgagt aaagtgacag cgggtgtgtac tgctgcccga tagaagtgcc tggtgtgttc 360
 aacgatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac caccgacaga 420
 acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480
 acaacaaccc cagctgcact tccaacaaca gtcgtgacca caccgcatct cacaaccgga 540
 acaccactcc agatgacaac cattgccgtc ttcacaacag caaacacgtg ccttttacta 600
 accccaagca cccttcggga ggaagccaca ggtcttctga ctcccagacc ttctaaggaa 660
 gggcccatcc tcactgcaga atcagaaact gtcctcccca gtgattcctg gtagtagtct 720
 gagtctactt ctgctgacac tgtcctgctg acatccaaag agtccaaagt ttgggatctc 780
 ccatcaacat cccacgtgtc aatgtggaaa acgagtgatt ctgtgtcttc tcctcagcct 840

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ggagcatctg atacagcagt tcctgagcag aacaaaacaa caaaaacagg acagatggat 900
ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgat gatcatcgcc 960
ccctccttgg gatttgtgct cticgcattg tttgtggcgt ttctcctgag agggaaactc 1020
atggaaacct attgttcgca gaaacacaca aggctagact acattggaga tagtaaaaat 1080
gtcctcaatg acgtgcagca tggaagggaa gacgaagacg gcctttttac cctctaacaa 1140
cgcagtagca tgttag                                     1156

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<210> 35
<211> 378
<212> PRT
<213> H. sapiens

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<220>
<221> VARIANT
<222> (1)...(378)
<223> TIM-4, allele 2

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<400> 35
Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
 1      5      10      15
Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
 20      25      30
Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
 35      40      45
Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
 50      55      60
Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
 65      70      75      80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
 85      90      95
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
 100     105     110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
 115     120     125
Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
 130     135     140
Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met
 145     150     155     160
Thr Thr Thr Pro Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
 165     170     175
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
 180     185     190
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
 195     200     205
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
 210     215     220
Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Val
 225     230     235     240
Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys
 245     250     255
Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser
 260     265     270
Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro
 275     280     285
Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met
 290     295     300
Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala
 305     310     315     320
Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu
 325     330     335
Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu

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	340		345		350
Asp Tyr Ile	Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly				
	355		360		365
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu					
	370		375		

<210> 36
 <211> 1156
 <212> DNA
 <213> H. sapiens

<400> 36

atgtccaaag	aacctctcat	tctctggctg	atgattgagt	tttgggtggct	ttacctgaca	60
ccagtcactt	cagagactgt	tgtgacggag	gttttgggtc	accgggtgac	tttgccctgt	120
ctgtactcat	cctggtctca	caacagcaac	agcatgtgct	gggggaaaga	ccagtgcgcc	180
tactccggtt	gcaaggaggc	gtcatccgc	actgatggaa	tgagggtgac	ctcaagaaag	240
tcagcaaaat	atagacttca	ggggactatc	ccgagagggtg	atgtctcctt	gaccatctta	300
aacccccagt	aaagtgacag	cggtgtgtac	tgctgccgca	tagaagtgcc	tggttggttc	360
aacgatgtaa	agataaacgt	gcgcctgaat	ctacagagag	cctcaacaac	cacgcacaga	420
acagcaacca	ccaccacacg	cagaacaaca	acaacaagcc	ccaccaccac	ccgacaaatg	480
acaacaaccc	cagctgcact	tccaacaaca	gtcgtgacca	caccgatct	cacaaccgga	540
acaccactcc	agatgacaac	cattgccgtc	ttcacaacag	caaacacgtg	cctttcacta	600
accccaagca	cccttcgga	ggaagccaca	ggtcttctga	ctcccgagcc	ttctaaggaa	660
gggcccattc	tactgcaga	atcagaaact	gtcctcccca	gtgattcctg	gagtagtggt	720
gagtctactt	ctgctgacac	tgtcctgctg	acatccaaag	agtccaaagt	ttgggatctc	780
ccatcaacat	cccacgtgtc	aatgtggaaa	acgagtgatt	ctgtgtcttc	tcctcagcct	840
ggagcatctg	atacagcagt	tcctgagcag	aacaaaacaa	caaaaacagg	acagatggat	900
ggaataccca	tgtcaatgaa	gaatgaaatg	cccatctccc	aactactgat	gatcatcgcc	960
ccctccttgg	gatttgtgct	cttcgcattg	tttgtggcgt	ttctcctgag	agggaaactc	1020
atggaaacct	attgttcgca	gaaacacaca	aggctagact	acattggaga	tagtaaaaat	1080
gtcctcaatg	acgtgcagca	tggaaggga	gacgaagacg	gcctttttac	cctctaacaa	1140
cgcagtagca	tgtag					1156

<210> 37
 <211> 481
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(430)
 <223> Exon 3, reference sequence

<400> 37

ttctagctgg	gcaatgacca	agattgacag	ttcaggaagt	taactccacc	tagggacagt	60
ctgtcattgg	tgtgctaggg	tacagttcca	gcctgaggct	cttgtttctt	gtttgactta	120
tgctcactct	catgttgatt	tctgactcca	gccaagggtca	cgactactcc	aattgtcaca	180
actgttccaa	ccgtcacgac	tggtcgaacg	agcaccactg	ttccaacgac	aacgactgtt	240
ccaacgacaa	ctgttccaac	aacaatgagc	attccaacga	caacgactgt	tctgacgaca	300
atgactgttt	caacgacaac	gagcgttcca	acgacaacga	gcattccaac	aacaacaagt	360
gttccagtga	caacaactgt	ctctaccttt	gttcctccaa	tgcttttgcc	caggcagaac	420
catgaaccag	gtaaaacaga	tgtgtttgga	agcccaaagg	ccttctaata	aggagctgcg	480
g						481

<210> 38
 <211> 499
 <212> DNA
 <213> H. sapiens

<220>

<221> exon
 <222> (152)...(448)
 <223> Exon 3, INS157 polymorphism

<400> 38
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgtttccaa ccgtcacgac tggttcgaac agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
 acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc 360
 attccaacaa caacaagtgt tccagtgaac acaactgtct ctacctttgt tcttccaatg 420
 cctttgcccc ggcagaacca tgaaccaggt aaaacagatg tgtttggaag cccaaaggcc 480
 ttctaataag gagctgcgg 499

<210> 39
 <211> 496
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(445)
 <223> Exon 3, 195delT polymorphism

<400> 39
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgtttccaa ccgtcacgac tggttcgaac agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
 acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc 360
 attccaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
 ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc 480
 taatgaggag ctgcgg 496

<210> 40
 <211> 496
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(445)
 <223> Exon 3, 157insMTTVP polymorphism

<400> 40
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgtttccaa ccgtcacgac tggttcgaac agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacga ctgtttccaac gacaactgtt ccaacaacaa tgagcattcc aacgacaacg 300
 actgtttctga cgacaatgac tggtttcaacg acaacgagcg ttccaacgac aacgagcatt 360
 ccaacaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
 ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc 480
 taatgaggag ctgcgg 496

<210> 41
 <211> 18
 <212> DNA

<213> H. sapiens
 <400> 41
 gtgtctgaca gtggcgta 18
 <210> 42
 <211> 18
 <212> DNA
 <213> H. sapiens
 <400> 42
 ttgcccagg cagaacca 18
 <210> 43
 <211> 18
 <212> DNA
 <213> H. sapiens
 <400> 43
 ccaccaagg tcacgact 18
 <210> 44
 <211> 18
 <212> DNA
 <213> H. sapiens
 <400> 44
 atgccacgga ctaagacc 18
 <210> 45
 <211> 41
 <212> DNA
 <213> H. sapiens
 <400> 45
 ggaattcgtc gaccaccatg catcctcaag tggatcatctt a 41
 <210> 46
 <211> 42
 <212> DNA
 <213> H. sapiens
 <400> 46
 ggaattcgcg gccgctcatt agtcctgggc ataaacagta tt 42
 <210> 47
 <211> 20
 <212> DNA
 <213> H. sapiens
 <400> 47
 tcaagtggtc atcttaagcc 20
 <210> 48
 <211> 22
 <212> DNA
 <213> H. sapiens
 <400> 48
 taaactctca aagagcacca ct 22

<210> 49
 <211> 22
 <212> DNA
 <213> H. sapiens

 <400> 49
 acagactcca gcatagattc ct 22

 <210> 50
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 <212> DNA
 <213> H. sapiens

 <400> 50
 gcaccaagac agaaatacag ac 22

 <210> 51
 <211> 31
 <212> DNA
 <213> H. sapiens

 <400> 51
 agaagcaccc aagacagaaa tacagactcc a 31

 <210> 52
 <211> 19
 <212> DNA
 <213> H. sapiens

 <400> 52
 ttctagctgg gcaatgacc 19

 <210> 53
 <211> 20
 <212> DNA
 <213> H. sapiens

 <400> 53
 ccgcagctcc tcattagaag 20